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FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGGAGAGTAACAGCAGCCACACGTGCATGCCC
CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC
TTCCTCGCCGCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG
CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG
ATTTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAAC
ACCATTGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG
TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC
CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT
CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTC
ATCGTCATTCCACTGATTGTCAATGATTGCCTGCTACTCCGTGGTGGTCTGTGCAGCCCG
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCAGGATGAGAGT
GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG
GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCC
AGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT
AAGGAAGGCAGCACCAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTTCGCACAGAG
GTCAACCAGTGACGATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC
AATTTCACTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCCACCCAGTCGT
CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTG
ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTTAGCAGTC
CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC
TGGCTTTTCTTCTGCACTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA
GAAGATAGCCACCCAGACCTGCCCCGGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT
TCCTACGATTCTGCTACTTTTCTCTGA

FIG. 2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLQRKP
QLLQVTNRFI FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPPLYGWGQAAFDERNA
LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
CVENEDEEGAEEKKEEFQDESEFRQHEGEVKAKEGRMEAKDGSLLAKEGSTGTSESSVEA
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYQCKAAKVI FIIIFSYVLSLGPYCFLAV
LAVWVDVETQVPQWVITII IWLFFLQCCIHYPVYGYMHKTIKKEIQDMLKKFFCKEKKPPK
EDSHPDLPGTEGGTEGKIVPSYDSATFP

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1	MTSTCTNSTR	ESNSSHTCMP	LSKMPISLAH	GIIRST	<u>VLVI</u>	<u>FLAASFVGNI</u>
51	<u>VLALVL</u> QRKP	QLLQVTNRFI	<u>FNLLVTDLLQ</u>	<u>ISLVAPWVVA</u>	<u>TSVPLEFWPLN</u>	
101	<u>SHFCTALVSL</u>	<u>THLFAFASVN</u>	<u>TIVLVSVD</u> RY	LSIIHPLSYP	SKMTQRRGYL	
151	<u>LLYGTWIVAI</u>	<u>LQSTPPLYGW</u>	GQAAFDERNA	LCSMIWGASP	SYT <u>ILSVVSF</u>	
201	<u>IVIPLIVMIA</u>	<u>CYSVVFCAAR</u>	RQHALLYNVK	RHSLEVRVKD	CVENEDEEGA	
251	EKKEEFQDES	EFRRQHEGEV	KAKEGRMEAK	DGSLKAKEGS	TGTSESSVEA	
301	RGSEEVRESS	TVASDGSMEG	KEGSTKVEEN	SMKADKGRTE	VNQCSIDLGE	
351	DDMEFGEDDI	NFSEDDVEAV	NIPESLPPSR	RNSNSNPPLP	RCYQCKAAKV	
401	<u>IFIIIFS</u> YVL	<u>SLGPYCFLAV</u>	LAVWVDVETQ	VPQ <u>WVITIII</u>	<u>WLFFLQCCIH</u>	
451	<u>PYVYGYMHKT</u>	IKKEIQDMLK	KFFCKEKPPK	EDSHPDLPGT	EGGTEGKIVP	
501	SYDSATFP					

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FIG. 6A

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~MANFTFGDLALDVARMGGLASTPSGLRSTGLTTPGLSPT
A1AD_HUMAN	MTRDILLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
A1AD_MOUSE	MTRDILSVTFEGPRASSSTGGSGAGGGAGTVG...P.EG
Q13675	~~~~~
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	~~~~~
O54913	~~~~~
A1AA_BOVIN	~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	~~~~~
A1AA_HUMAN	~~~~~
A1AA_ORYLA	~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~MHNLSAQPWQAKMANITYDNVTLSN
YDBM_CAEEL	MCFAEKGEAGEDVDHHSFLC.P.KKLVGN...KGFIRN
5H1A_HUMAN	~~~~~MDV..LSPGQ...GNNTT...SPPAPFETGGN
5H1A_MOUSE	~~~~~MDM..FSLGQ...GNNTT...TSLEPFGTGGN
5H1A_FUGRU	~~~~~MDLRATSSND...SNATSGYSDTAAVDWDEGEN
5HT_LYMST	GLVTSDFNDSYGLT.GQFINGSHSSRSRDNASANDTSATN
A1AD_HUMAN	PAVGGVPGGAGGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
A1AD_MOUSE	PAVGGVP.GATGGSAVVGTGSGEDNQSSAEAGAA.ASGE
Q13675	~~~~~MVFLSGNASDS
Q13729	~~~~~MVFLSGNASDS
O60451	~~~~~MVFLSGNASDS
A1AA_RAT	~~~~~MVLLSENASEG
O54913	~~~~~MVLLSENASEG
A1AA_BOVIN	~~~~~MVFLSGNASDS
A1AA_CANFA	~~~~~MVFLSGNASDS
A1AA_RABIT	~~~~~MVFLSGNASDS
A1AA_HUMAN	~~~~~MVFLSGNASDS
A1AA_ORYLA	~~~~~MTPSSVTLNC
O96716	~~~~~MSANTTVSPTETTANTANSTEA
O75963	~~~~~MSLNSSLS
HGPRBMY8	~~~~~MTSTCTNSTRESNS

FIG. 6B

ACM4_CHICK	RSEVAIQPPTNYKTVELMFLATVTGSLS..LVTVVGNILV
YDBM_CAEEL	QYH.....QHETIQ..ILKGSALFLLV..LWTIFANSLV
5H1A_HUMAN	ITG...ISDVTVSYQ..VITSLLLGTLL..FCAVLGNACV
5H1A_MOUSE	DTG...LSNVTFYSYQ..VITSLLLGTLL..FCAVLGNACV
5H1A_FUGRU	ATGSGSLPDEEFSYQ..IITSIFLGALI..LCSTIFGNSCV
5HT_LYMST	MTDDRYWSLTVYSHEHLVLTSVILGLFV..LCCITIGNCFV
A1AD_HUMAN	V..NGTAAVGGGLVVSAGVGVGVLAAFI..LMAVAGNLLV
A1AD_MOUSE	V..NGSAAVGGGLVVSAGVGVGVLAAFI..LTAVAGNLLV
Q13675	S..NCTQPPAP..VNISKAILLGVILGGLI..LFGVLGNILV
Q13729	S..NCTQPPAP..VNISKAILLGVILGGLI..LFGVLGNILV
O60451	S..NCTQPPAP..VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_RAT	S..NCTHPPAP..VNISKAILLGVILGGLI..IFGVLGNILV
O54913	S..NCTHPPAQ..VNISKAILLGVILGGLI..IFGVLGNILV
A1AA_BOVIN	S..NCTHPPPP..VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_CANFA	S..NCTHPPAP..VNISKAILLGVILGGLI..IFGVLGNILV
A1AA_RABIT	S..NCTHPPAP..VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_HUMAN	S..NCTQPPAP..VNISKAILLGVILGGLI..LFGVLGNILV
A1AA_ORYLA	S..NCSHVLAPELNTVKAVVLGMVLGIFI..LFGVIGNILV
O96716	SVGSCFAPNPYSAGVOAV..LGLITVILI..LLTVIGNVLV
O75963	CRKELSNLTEEEGGEGGVITQFIATIVITIEFVCLGNLVI
HGPRBMY8	SHTCMPLSKMPTSLAHGITRSTVL..VIFLAASFVGNIVL
ACM4_CHICK	MLSTIKVNRQLOTVNNYELFSLACADLITGVFSMNLYTVYI
YDBM_CAEEL	FLVLYKNPRLQTVPNLLVGNLAFSDLALGLIVLPLSSVYA
5H1A_HUMAN	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_MOUSE	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5H1A_FUGRU	VAAIALERSLQNVANYLIGSLAVTDLMVSVLVLPMAALYQ
5HT_LYMST	IAAVMLERSLHNVANLYLISLAVADLMVAVLVMPLSVVSE
A1AD_HUMAN	ILSVACNRHLOTVTNFYIVNLAVADLLLSATVLPFSATME
A1AD_MOUSE	ILSVACNRHLOTVTNFYIVNLAVADLLLSAAVLPFSATME
Q13675	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
Q13729	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
O60451	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_RAT	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
O54913	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_BOVIN	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_CANFA	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_RABIT	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_HUMAN	ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFE
A1AA_ORYLA	ILSVVCHRHLQTVTYFYIVNLAVADLLLSSTVLPFSAIFE
O96716	ILAVTCHRKMRVTNFFIVSLACADLSVGITVLPFAATND
O75963	VVTLYKKSYLELTLNKFVFSLTLSNFLLSVLVLPFVVTSS
HGPRBMY8	ALVLRQKPQLLOVTNREFIENLLVTDLLQISLVAPWVATS

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FIG. 6C

ACM4_CHICK	IKGYWPLGAVVCDLWLALDYVVSNASVMNLLTISFD	RYFC
YDBM_CAEEL	IAGEWVEPDALCEVVSADILCSTASIWNLSIVGL	DRYWA
5H1A_HUMAN	VLNKWTLGQVTCDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5H1A_MOUSE	VLNKWTLGQVTCDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5H1A_FUGRU	VLNKWTLGQDICDLFIALDVLCCCTSSILHLCAIAL	DRYWA
5HT_LYMST	ISKVWFLHSEVCDMWISVDVLCCTASILHLVAIAM	DRYWA
A1AD_HUMAN	VLGEWAFGRAFCDVWAADVLCCTASILSLCTISV	DRYVG
A1AD_MOUSE	VLGEWPFGRTEFCDVWAADVLCCTASILSLCTISV	DRYVG
Q13675	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
Q13729	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
O60451	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RAT	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
O54913	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_BOVIN	ILGYWAFGRVFCNVWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_CANFA	ILGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_RABIT	ILGYWAFGRVFCNIWAAVDVLCCTASISLCLVIS	DRYIG
A1AA_HUMAN	VLGYWAFGRVFCNIWAAVDVLCCTASIMGLCTIS	DRYIG
A1AA_ORYLA	ILDRWVFGRVFCNIWAAVDVLCCTASIMSLCLVIS	DRYIG
O96716	ILGYWPFGG.YCDVWVSFDVLNSTASILNLVVI	AFDRELA
O75963	IRREWIFGVVWCNFSALLYLLISSASMTLGVIA	TDRIYA
HGPRBMY8	VPLFWPLNSHECTALVSLTHLFAFASVNTIVLV	SVDRYLS
ACM4_CHICK	VTKPLTYPARRTTKMAGLMTAAAWTISFILWAPAT	.LFW.
YDBM_CAEEL	ITSPVAYMSKRNKRTAGIMTISVWISSALISLAPL	.LGWK
5H1A_HUMAN	ITDPIDYVNKRTPRRAAALTSLTWLTIGFLISIPP	.LGW.
5H1A_MOUSE	ITDPIDYVNKRTPRRAAALTSLTWLTIGFLISIPP	.LGW.
5H1A_FUGRU	ITDPIDYVNKRTPRRAAVLISVTWLTIGFSISIPP	.LGW.
5HT_LYMST	VTS.IDYIRRRSARRILMTMVVWIVAFISIPPL	.FGW.
A1AD_HUMAN	VRHSLKYPAIMTERKAAAILALTWVVALVVS	VGPL.LGW.
A1AD_MOUSE	VRHSLKYPAIMTERKAAAILALTWVVALVVS	VGPL.LGW.
Q13675	VSYPTRYPTIIVTQRRGLMALLCVWALS	SLVISIGPL.FGW.
Q13729	VSYPTRYPTIIVTQRRGLMALLCVWALS	SLVISIGPL.FGW.
O60451	VSYPTRYPTIIVTQRRGLMALLCVWALS	SLVISIGPL.FGW.
A1AA_RAT	VSYPTRYPTIIVTQRRGVRAALCVWALS	SLVISIGPL.FGW.
O54913	VSYPTRYPTIIVTQRRGVRAALCVWALS	SLVISIGPL.FGW.
A1AA_BOVIN	VSYPTRYPTIIVTQKRGMLALLCVWALS	SLVISIGPL.FGW.
A1AA_CANFA	VSYPTRYPTIIVTQKRGMLALLCVWALS	SLVISIGPL.FGW.
A1AA_RABIT	VSYPTRYPTIIVTQRRGLRALLCVWAFSLVIS	VGPL.FGW.
A1AA_HUMAN	VSYPTRYPTIIVTQRRGLMALLCVWALS	SLVISIGPL.FGW.
A1AA_ORYLA	VSYPTRYPAIMTKRRALLEAVMLLWVLSV	ISIGPL.FGW.
O96716	ITAPFTYHTRMTERTAGILLATVWGTSLV	VSFLPQAGWY
O75963	VLYPMVYPMKTTGNRAVMALVYIWLHSL	IGCLPPL.FGWS
HGPRBMY8	TIHPLSYPSKMTQRRGYLLLYGTWLVATL	QSTPPL.YGWG

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FIG. 6D

ACM4_CHICK	QFIVGKRTVHE.....RECYIQFLSNPAVTFGTAIAAFYL
YDBM_CAEEL	QTAQTENLIYEKNNTVRQC..TFLDLPSYTVYSATGSFFI
5H1A_HUMAN	R.TP.EDRSDPDA.....CTIS..KDHGYTIYSTFGAFYI
5H1A_MOUSE	R.AP.EDRSNPNE.....CTIS..KDHGYTIYSTFGAFYI
5H1A_FUGRU	R.SA.EDRANPDA.....CIIS..QDPGYTIYSTFGAFYI
5HT_LYMST	R.DPNNDPDKTGT.....CIIS..ODKGYTIYSTFGAFYI
A1AD_HUMAN	K.EPVPP.....DERFCGIT..EEAGYAVFSSVCSFYI
A1AD_MOUSE	K.EPVPP.....DERFCGIT..EEVGYATFSSVCSFYI
Q13675	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYI
Q13729	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYI
O60451	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYI
A1AA_RAT	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
O54913	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_BOVIN	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_CANFA	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_RABIT	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYV
A1AA_HUMAN	R.QPAPE.....DETICQIN..EPPGYVLFSAIGSFYI
A1AA_ORYLA	K.EPAPE.....DETICKIT..EPPGYATFSAIGSFYI
O96716	R.DNQSEALAIYSDPCLCIFT..ASTAYTIVSSILISFYI
O75963	S.VEFDEFKWM.....CVAAWH..REPGYTAFWQIWCALF
HGPRBMY8	QA.....AFDERNALCSMIWGASPSYTIILSVVSFIVI
ACM4_CHICK	PVIMTVLYIHTSTA.SRSRVRRHKPESRKERKGSLSFF
YDBM_CAEEL	PTLLMFFVYFKIYQAFAKHRAQIYRQKVIRKHIESTILH
5H1A_HUMAN	PLLEMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_MOUSE	PLLEMLVLYGRIFRA.....ARFRIRKTVKKVEK.....
5H1A_FUGRU	PLLEMLVLYGRIFKA.....ARFRIRKTVKKTEKA.....
5HT_LYMST	PMLVMMTIYIRLWLV.....ARSRIKDKFQMTKARL...
A1AD_HUMAN	PMVAVIVMYCRVYVV.....A.....RSTTRSL...
A1AD_MOUSE	PMVAVIVMYCRVYVV.....A.....RSTTRSL...
Q13675	PLAILVLMYCRVYVV.....A.....KRESRGL...
Q13729	PLAILVLMYCRVYVV.....A.....KRESRGL...
O60451	PLAILVLMYCRVYVV.....A.....KRESRGL...
A1AA_RAT	PLAILVLMYCRVYVV.....A.....KRESRGL...
O54913	PLTIILVLMYCRVYVV.....A.....KRESRGL...
A1AA_BOVIN	PLTIILVLMYCRVYVV.....A.....KRESRGL...
A1AA_CANFA	PLTIILVLMYCRVYVV.....A.....KRESRGL...
A1AA_RABIT	PLTIILVLMYCRVYVV.....A.....KRESRGL...
A1AA_HUMAN	PLAILVLMYCRVYVV.....A.....KRESRGL...
A1AA_ORYLA	PLAILVLMYCRVYVV.....A.....OKESRGL...
O96716	PLLIIMLVFYGITFEKA.....A.....RDQARKI...
O75963	PFLVMLVCYGFIERV.....ARV.....KARKV...
HGPRBMY8	PLIIMTIACYSVVECAARRQHA.LLYNVKRHSLEVRVKDCV

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FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	SPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL	EISHVLPTSDE	FAKEEEEEEDSESSGQVENGLGNGNDAI.
5H1A_HUMAN	TGADTRHGASPAQPK..KSVNG....E..
5H1A_MOUSE	KGAGTSFGTSSAPPPK..KSLNG....Q..
5H1A_FUGRU	KASDMCLTLSPAVFHK..RA.NG....D..
5HT_LYMST	KTEETTLVASPKTEYSVVSDCNGCNSPD..
A1AD_HUMAN	EA.....GVKRER..
A1AD_MOUSE	EA.....GIKREP..
Q13675	KS.....GLKTDK..
Q13729	KS.....GLKTDK..
O60451	KS.....GLKTDK..
A1AA_RAT	KS.....GLKTDK..
O54913	KS.....GLKTDK..
A1AA_BOVIN	KS.....GLKTDK..
A1AA_CANFA	KS.....GLKTDK..
A1AA_RABIT	KS.....GLKTDK..
A1AA_HUMAN	KS.....GLKTDK..
A1AA_ORYLA	KE.....GQKIEK..
O96716	NA.....LEG....
O75963	HCGTVVIVEEDAQRTGRKNSSTSTSSSG..
HGPRBMY8	ENEDEEGAEEK	EEFQDESEFRRQHEGEVKAKEGRMEAKDG
ACM4_CHICK	QQEEKETS	SNESSTVSMTQTTKDKPTTEILPAGQGQSPAHP
YDBM_CAEEL	.IEEDE	CEDEDSDEKRDDHTS...MTTVTATVTGPTEA.P
5H1A_HUMAN	..SGSR	NWRLGVESKAGGALCANGAVRQGDDGAAL.EVIE
5H1A_MOUSE	..PGSG	DCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE
5H1A_FUGRU	..AVSA	EWKRGYKFKP..SSPCANGAVRHGEEMESL.EVIE
5HT_LYMST	..STEK	KKRRAPFKSYG..CSPRPERKKNRAKKLPEAN
A1AD_HUMAN	..GKASEVVL
A1AD_MOUSE	..GKASEVVL
Q13675	..SDSEQVTL
Q13729	..SDSEQVTL
O60451	..SDSEQVTL
A1AA_RAT	..SDSEQVTL
O54913	..SDSEQVTL
A1AA_BOVIN	..SDSEQVTL
A1AA_CANFA	..SDSEQVTL
A1AA_RABIT	..SDSEQVTL
A1AA_HUMAN	..SDSEQVTL
A1AA_ORYLA	..SDSEQVIL
O96716
O75963	..SRRNA	FQGVVYSANQCKALITILVVLGAFMVTWGPYMV
HGPRBMY8	SLKAKE	GSTGTSESSVEARGSEEVRRESSTVASDGSMEGKE

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FIG. 6F

ACM4_CHICK	RVNPTSKWSKIKIVTKQTGTESVTAIEIVPAKAGASDHNS
YDBM_CAEEL	YMKREAKISKSVPIEKESAIQKREAKPMRSVMAISYEKVK
5H1A_HUMAN	.VHRVGNSKEHLPL....PSEAGPT....PCAP....ASF
5H1A_MOUSE	.VHRVGNSKGDPL....PSESGAT....SYVP....ACL
5H1A_FUGRU	.VN..SNSKTHLPL....PN....T....P.QS....SSH
5HT_LYMST	GVNSNSSSSERLKQIQIETAEAFAN....GCAEEASTAML
A1AD_HUMAN	RIHC.....RGAAT....GADGAHGMRSA
A1AD_MOUSE	RIHC.....RGAAT....SAKGNPGTQSS
Q13675	RIHR.....KNAPA.....GGSGMASA
Q13729	RIHR.....KNAPA.....GGSGMASA
O60451	RIHR.....KNAPA.....GGSGMASA
A1AA_RAT	RIHR.....KNVPA.....EGGGVSSA
O54913	RIHR.....KNVPA.....EGSGVSSA
A1AA_BOVIN	RIHR.....KNAQV.....GGSGVTSA
A1AA_CANFA	RIHR.....KNAPV.....GGTGVSSA
A1AA_RABIT	RIHR.....KNAPA.....GGSGVASA
A1AA_HUMAN	RIHR.....KNAPA.....GGSGMASA
A1AA_ORYLA	RMHR.....GNTTV.....SEDEAL
O96716	RLEQ.....EN.....NRGKKISLA
O75963	VI...ASEALWGKSSVSPSLETWAT....WLSFASAVCHP
HGPRBMY8	GSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDINF
ACM4_CHICK	LSNSRPANVARKFASTARSQVRKKROMAAR..EKKVTRTI
YDBM_CAEEL	RHKNRKERIYRK..SLQR...KPKAISAAK..ERRGVKVL
5H1A_HUMAN	ERK..NERN.....AEAKRKMA..LAR..ERKTVKTL
5H1A_MOUSE	ERK..NERT.....AEAKRKMA..LAR..ERKTVKTL
5H1A_FUGRU	ENI..NEKT.....TGTRRKIA..LAR..ERKTVKTL
5HT_LYMST	ERQCNGGKKISSNDTPYSRTREKLE..LKR..ERKAAKTL
A1AD_HUMAN	KG.....HTFRSSLV.....RLLK..FSR..EKKA AKTL
A1AD_MOUSE	KG.....HTLRSSLV.....RLLK..FSR..EKKA AKTL
Q13675	KT.....KT...HFSV.....RLLK..FSR..EKKA AKTL
Q13729	KT.....KT...HFSV.....RLLK..FSR..EKKA AKTL
O60451	KT.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_RAT	KN.....KT...HFSV.....RLLK..FSR..EKKA AKTL
O54913	KN.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_BOVIN	KN.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_CANFA	KN.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_RABIT	KN.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_HUMAN	KT.....KT...HFSV.....RLLK..FSR..EKKA AKTL
A1AA_ORYLA	RS.....RT...HFAT.....RLLK..FSR..EKKA AKTL
O96716	K.....K.....EKKA AKTL
O75963	LIYGLWNKTVRKELLGMCFGDRYYREFVQ..RORTSRLEF
HGPRBMY8	SEDDVEAVNIPESLPPSRNSNS.NPPLPRCYQCKAAKVI

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FIG. 6G

ACM4_CHICK	FATLLAFILTWTPYNMVLINTFC..ETCVPET.VWSIGY
YDBM_CAEEL	GIILGCFTVCWAPFFTMYVLVQFC..KDCSPNAHIEMFIT
5H1A_HUMAN	GIIMGTFILCWLPPFFIVALVLPE.CESSCHMPTLLGAIIN
5H1A_MOUSE	GIIMGTFILCWLPPFFIVALVLPE.CESSCHMPELLGAIIN
5H1A_FUGRU	GIIMGTFTFCWLPPFFIVALVLPE.CAENCYMPEWLGAVIN
5HT_LYMST	AIITGAFLICWLPPFFIALIGPE.VDPE.GIPPFARSEVL
A1AD_HUMAN	AIVVGVFVLCWFPPFFVLPGLSL.F.POLKPSEGVFKVIF
A1AD_MOUSE	AIVVGVFVLCWFPPFFVLPGLSL.F.POLKPSEGVFKVIF
Q13675	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPSETVFKIVF
Q13729	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPSETVFKIVF
O60451	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPSETVFKIVF
A1AA_RAT	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPSETVFKIVF
O54913	GIVVGC FVLCWLPPFFLVMPIGSF.F.PNFKPPETVFKIVF
A1AA_BOVIN	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFRPPSETVFKIAF
A1AA_CANFA	GIVVGC FVLCWLPPFFLVMPIG~~~~~
A1AA_RABIT	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPETVFKIVF
A1AA_HUMAN	GIVVGC FVLCWLPPFFLVMPIGSF.F.PDFKPPSETVFKIVF
A1AA_ORYLA	GIVVGC FVLCWLPPFFLVLPIGSI.F.PAYRPSDTVFKITE
O96716	GIIMGVFILCWLPPF.VVNI VNP.F.CDRCVQPAVFIALT
O75963	SISNRITDLGLSPHLTALMAGGQPLGHSSSTGDTGFSQSQ
HGPRBMY8	FIIFSYVLSLGPYCFIAVT.AVWVDVETQVPQWVITIII
ACM4_CHICK	WLCYVNSTINPACYALCNATFKKTEKHLIMCOYRNIGTAR
YDBM_CAEEL	WLGYSNSAMNPIIYT VFNRDYQIALKRLFTSEKKPSSTSR
5H1A_HUMAN	WLGYSNSLLNPVIYAYFNKDFQNAFKKLIKCKFCRQ~~~~
5H1A_MOUSE	WLGYSNSLLNPVIYAYFNKDFQNAFKKLIKCKFCR~~~~
5H1A_FUGRU	WLGYSNSLLNPVIYAYFNKDFQSAFKKILRCKFHRH~~~~
5HT_LYMST	WLGYNENLLNPVIYTFISPEFRSAFQKILFGKYRRGHR~~
A1AD_HUMAN	WLGYNENSCVNPLIYPCSSREFKRAFLRLRLC.QCRRRRR.
A1AD_MOUSE	WLGYNENSCVNPLIYPCSSREFKRAFLRLRLC.QCRRRRR.
Q13675	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
Q13729	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
O60451	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
A1AA_RAT	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RRQS
O54913	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RRQS
A1AA_BOVIN	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
A1AA_CANFA	~~~~~
A1AA_RABIT	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
A1AA_HUMAN	WLGYNENSCINPIIYPCSSQEFKKAFQNVLR.I.QCLR RKQS
A1AA_ORYLA	WLGYNENSCINPIIYLCSNQEFKKAFQSLGV.HCLRMTPR
O96716	WLGWINSCFNPIIY.AFNKEFRKVFVKMTCCHKCRGVTVG
O75963	DSGNLRAL~~~~~
HGPRBMY8	WLFELQCCIHPIYVYGYMHKTIKKEIQDMLKKFFCKEKPPK

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FIG. 6H

ACM4_CHICK	~~~~~
YDBM_CAEEL	V~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	.RRPLWRVY..GHHWRASTSGLRQDCAPSSGDAPPGAPLA
A1AD_MOUSE	.R..LW.....PSLRPPLAST..DRRPA LR LCPQPAHRT
Q13675	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
Q13729	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
O60451	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_RAT	SKH...ALG..YT.LHPPSQAVEGQHRDM.VRIPVGSGET
O54913	SKH...ALG..YT.LHPPSQAVEEQHRGM.VRIPVGSGET
A1AA_BOVIN	SKH...TLG..YT.LHAPSHVLEGGQHKDL.VRIPVGS AET
A1AA_CANFA	~~~~~
A1AA_RABIT	SKH...ALG..YT.LHAPSQALEGGQHKDM.VRIPVGSGET
A1AA_HUMAN	SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_ORYLA	AHHHHL SVG..QSQTQGHSLTISLDSKGAPCRLSPSSSVA
O96716	PNHADLNYDPVAMRLKKRGENANGTVNGDANGKANGNIEA
O75963	~~~~~
HGPRBMY8	EDSHPDLPGTEGGTEGKIVPSYDSATFP~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	LTALPDPD..PEP...PGTPEMQAPVASRRKPPSA...FR
A1AD_MOUSE	PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASLRLR
Q13675	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTART
Q13729	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARG
O60451	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARR
A1AA_RAT	FYKISKTDGVCEWKFFSSMPQGSARITV PKDQSACTTARV
O54913	FYKISKTDGVCEWKFFSSMPQGSARITMPKDQSACTTARV
A1AA_BOVIN	FYKISKTDGVCEWKIFSSLP RGSARMAVARDPSACTTARV
A1AA_CANFA	~~~~~
A1AA_RABIT	FYKISKTDGVCEWKFFSSMPRGSARITV PKDQSACTTARV
A1AA_HUMAN	FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARV
A1AA_ORYLA	LSRTPSSRDSREWRVFSGGPINSGL..PGPTEAGRAKVAKL
O96716	GEGTSSS~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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FIG. 6I

ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAAACQ
A1AD_MOUSE	EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675	KRSRVTRLECS...GMILAHCN..LRLPGSRDSPASASQ
Q13729	HT.PMT~~~~~
O60451	GMDCRYFTKNC...REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT	RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913	RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN	RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA	~~~~~
A1AA_RABIT	RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN	RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA	CNKSLHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSE
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~
ACM4_CHICK	~~~~~
YDBM_CAEEL	~~~~~
5H1A_HUMAN	~~~~~
5H1A_MOUSE	~~~~~
5H1A_FUGRU	~~~~~
5HT_LYMST	~~~~~
A1AD_HUMAN	RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE	RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675	AAGTTGDVPPGRRHQAQLIFVFLVETGFHHVGQDDLDDLLT
Q13729	~~~~~
O60451	~~~~~
A1AA_RAT	NGEEV~~~~~
O54913	NGEEV~~~~~
A1AA_BOVIN	NGEEV~~~~~
A1AA_CANFA	~~~~~
A1AA_RABIT	NGEEV~~~~~
A1AA_HUMAN	NGEEV~~~~~
A1AA_ORYLA	KGESV~~~~~
O96716	~~~~~
O75963	~~~~~
HGPRBMY8	~~~~~

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FIG. 6J

ACM4_CHICK	~
YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPRBMY8	~

FIG. 7

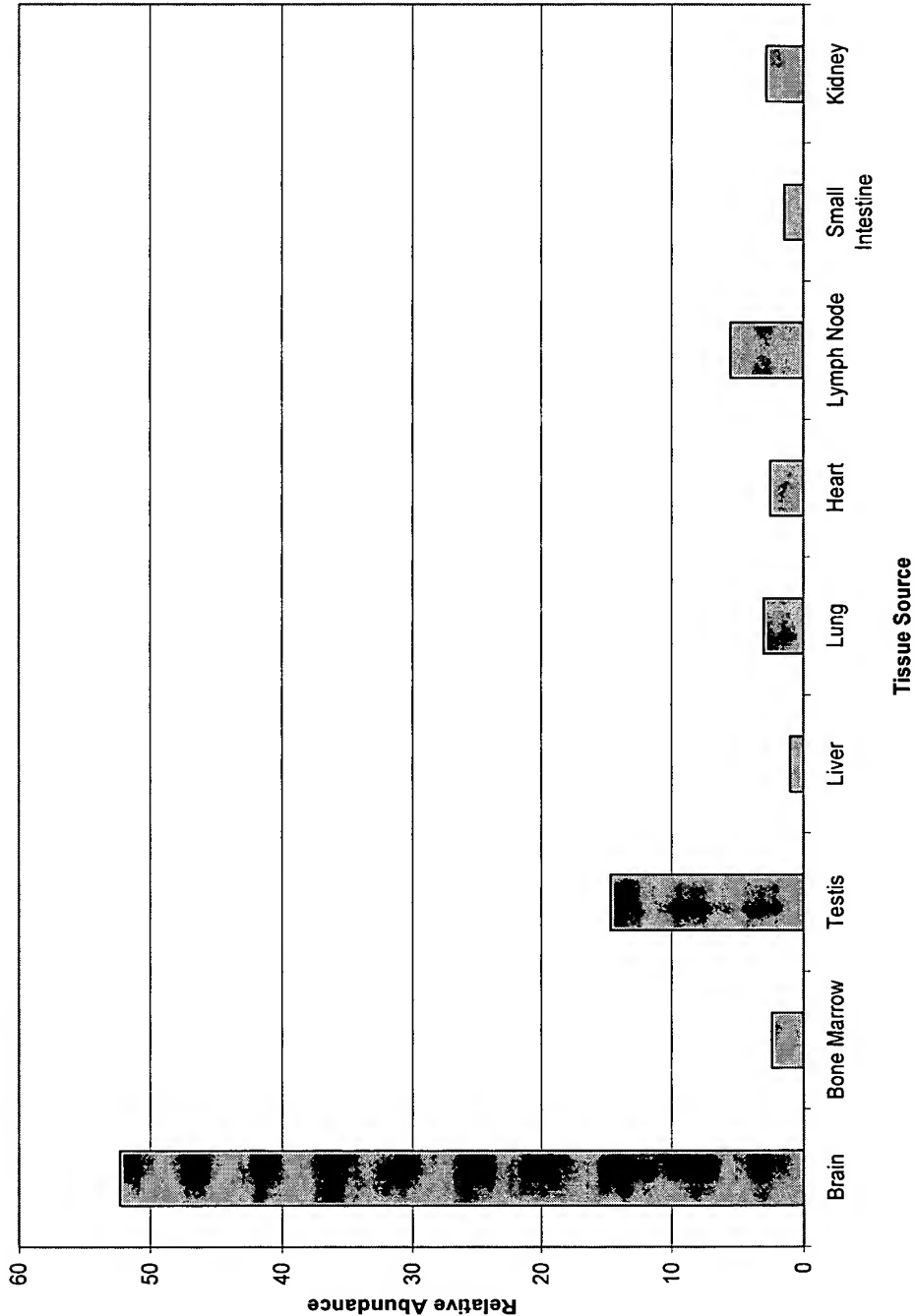
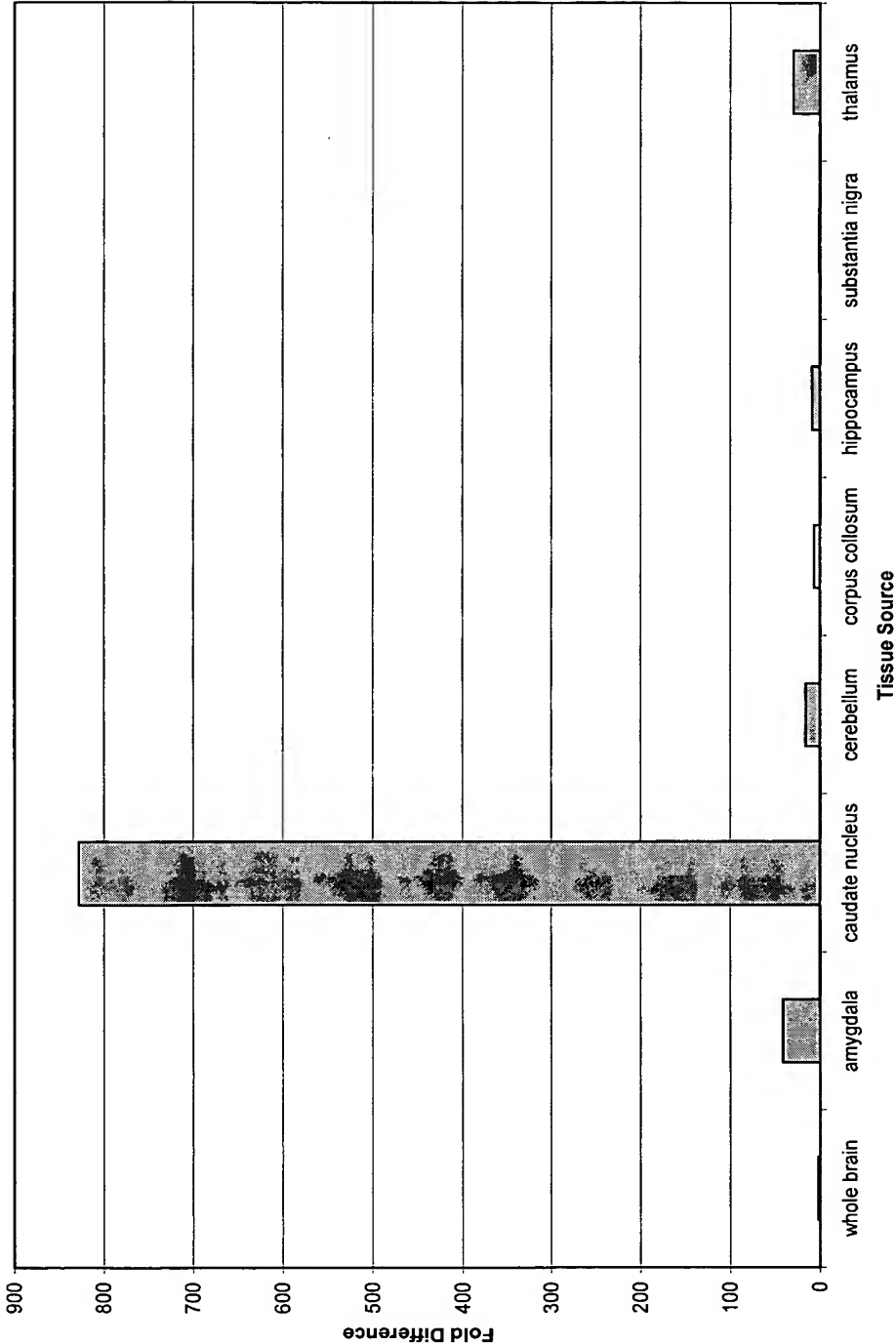


FIG. 8



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FIG. 9

HGPRBM8	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AL390879	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX148250	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX080495	MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
HGPRBM8	QLLQVTNRFIENLLVTDLLQISLVAPVWVATSVPFLWPLNSHFCTALVSLTHLFAFASVN
AL390879	QLLQVTNRFIENLLVTDLLQISLVAPVWVATSVPFLWPLNSHFCTALVSLTHLFAFASVN
AX148250	QLLQVTNRFIENLLVTDLLQISLVAPVWVATSVPFLWPLNSHFCTALVSLTHLFAFASVN
AX080495	QLLQVTNRFIENLLVTDLLQISLVAPVWVATSVPFLWPLNSHFCTALVSLTHLFAFASVN
HGPRBM8	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AL390879	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AX148250	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
AX080495	TIVVVSVDRLYSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAADFERN
HGPRBM8	LCSMIWGASPSYTIILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AL390879	LCSMIWGASPSYTIILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX148250	LCSMIWGASPSYTIILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX080495	LCSMIWGASPSYTIILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
HGPRBM8	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AL390879	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX148250	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
AX080495	CVENEDEEGAEEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
HGPRBM8	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AL390879	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX148250	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX080495	RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
HGPRBM8	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AL390879	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AX148250	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
AX080495	NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSIVLSLGPYCFLAV
HGPRBM8	LAVWVDVETQVPQWVITIIIWLFLLQCCIHPIVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AL390879	LAVWVDVETQVPQWVITIIIWLFLLQCCIHPIVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX148250	LAVWVDVETQVPQWVITIIIWLFLLQCCIHPIVYGYMHKTIKKEIQDMLKKFFCCKEPPK
AX080495	LAVWVDVETQVPQWVITIIIWLFLLQCCIHPIVYGYMHKTIKKEIQDMLKKFFCCKEPPK
HGPRBM8	EDSHPDLPGTEGGTEGKIVPSYDSATFP~
AL390879	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX148250	EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX080495	EDSHPDLPGTEGGTEGKIVPSYDSATFP*

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FIG. 10A

AX080495 GCCTGCAACCTGTCYCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
HGPRBMY8 ~~~~GCAACCTGTCCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
AL390879 ~~~~~~ATGACGTCCACCTGC
AX148250 ~~~~~~ATGACGTCCACCTGC

AX080495 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
HGPRBMY8 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AL390879 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC
AX148250 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCCTCTC

AX080495 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AL390879 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
AX148250 CAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
HGPRBMY8 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AL390879 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AX148250 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG

AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTGCTCGTGGCCCCCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
HGPRBMY8 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AL390879 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
AX148250 GCCCTGGTTAGCCTCACCCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
HGPRBMY8 TGTCTTGGTGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AL390879 TGTCTTGGTGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX148250 TGTCTTGGTGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC

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FIG. 10B

AX080495	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBM8	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250	TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX080495	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBM8	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250	GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX080495	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBM8	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250	GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX080495	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
HGPRBM8	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AL390879	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX148250	ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGGAGGCA
AX080495	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
HGPRBM8	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AL390879	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AX148250	GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCAGTCA
AX080495	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBM8	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250	AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX080495	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBM8	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250	TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX080495	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBM8	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250	CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX080495	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBM8	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250	GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX080495	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBM8	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250	GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA

FIG. 10C

AX080495	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250	AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX080495	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATG ¹ CATGGAGTTT
HGPRBMY8	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250	CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX080495	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AL390879	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX148250	GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX080495	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
HGPRBMY8	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AL390879	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AX148250	CCCCGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCCTCCTC
AX080495	TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8	TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
AL390879	TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
AX148250	TGCCCAGGTGCTACCAGTGCAAAGCT ² AAGAAAGTGATCTTCATCATCATT
AX080495	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
HGPRBMY8	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AL390879	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AX148250	TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AX080495	CGTGTGGGTGGATGTGCAAACCCAGGTACCCAGTGGGTGATCACCATAA
HGPRBMY8	CGTGTGGGTGGATGTGCAAACCCAGGTACCCAGTGGGTGATCACCATAA
AL390879	CGTGTGGGTGGATGTGCAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX148250	CGTGTGGGTGGATGTGCAAACCCAGGTACCCAGTGGGTGATCACCATAA
AX080495	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250	TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX080495	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250	TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX080495	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
HGPRBMY8	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AL390879	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AX148250	CTTCTGCAAGGAAAAGCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG

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FIG. 10D

```
AX080495 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
HGPRBMY8 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AL390879 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AX148250 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT

AX080495 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAATCAGTCCTTCA
HGPRBMY8 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~
AL390879 ACTTTTCCTTGA~~~~~
AX148250 ACTTTTCCTTGA~~~~~

AX080495 GCCACAGCTATTTAGAGCTTTAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8 ~~~~~
AL390879 ~~~~~
AX148250 ~~~~~

AX080495 CTTTCTGTG
HGPRBMY8 ~~~~~
AL390879 ~~~~~
AX148250 ~~~~~
```

FIG. 11

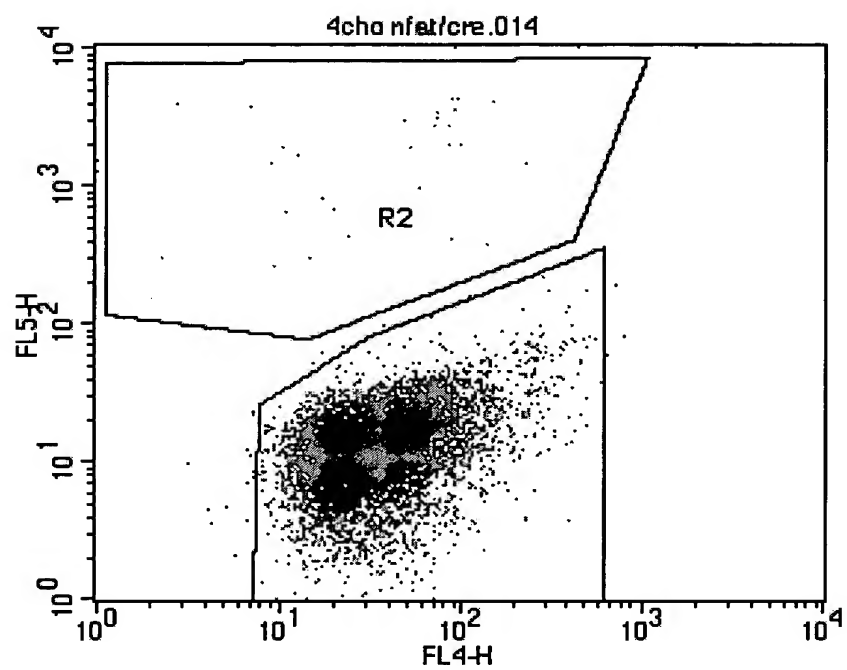
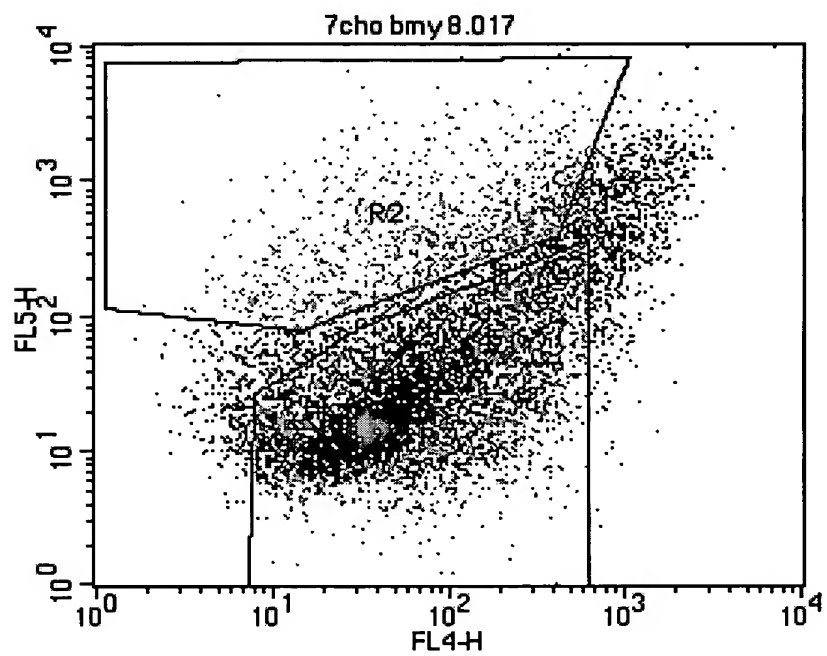


FIG. 12



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FIG. 13

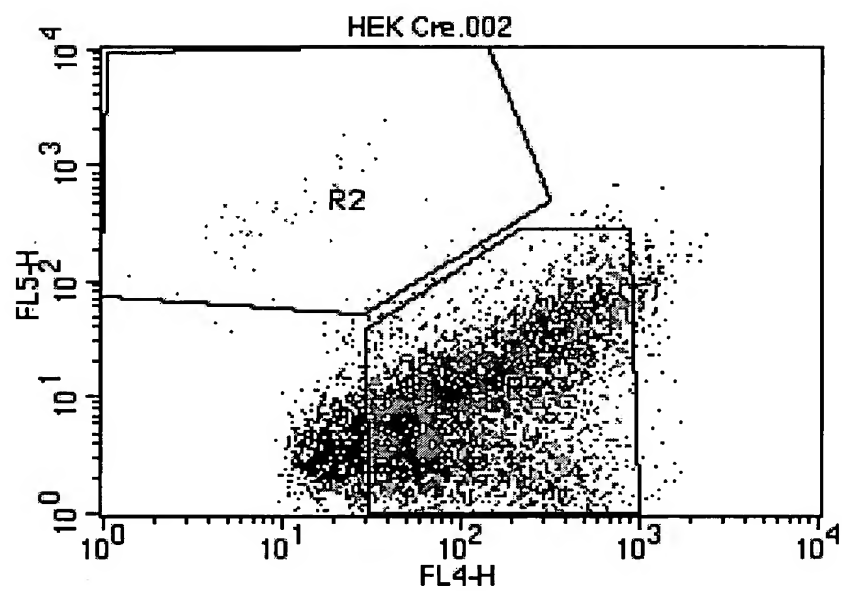
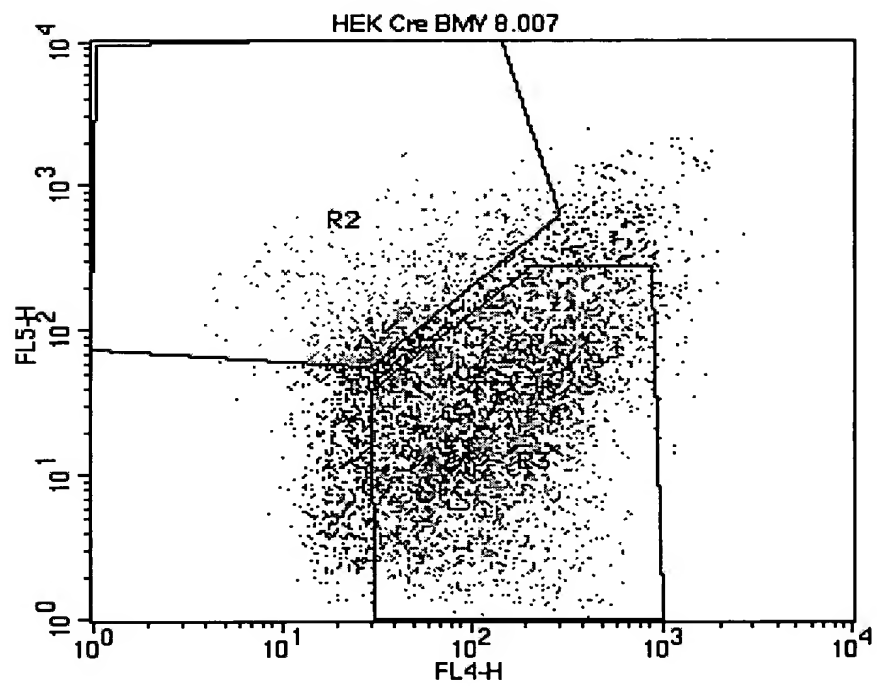


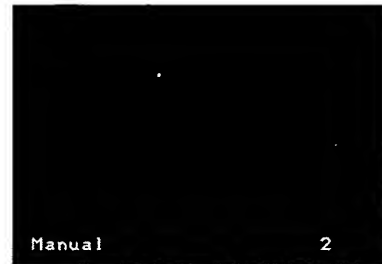
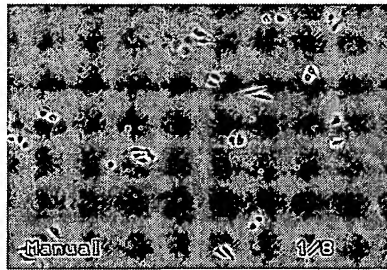
FIG. 14



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FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)

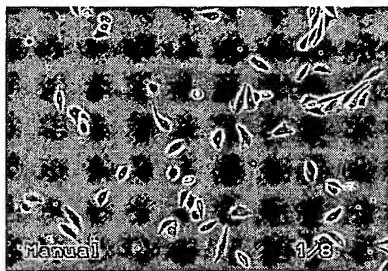
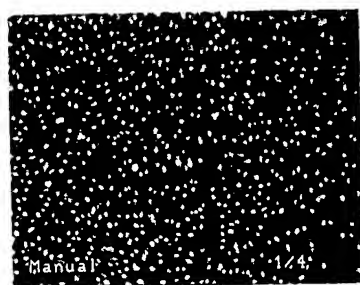
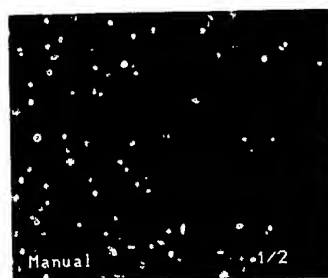


FIG. 16

a. CHO-NFAT CRE



b. CHO-NFAT/CRE + F.T.P



c. CHO-NFAT CRE oGPCR-Intermediate



d. CHO-NFAT/CRE oGPCR high

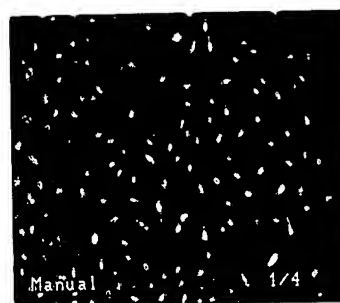
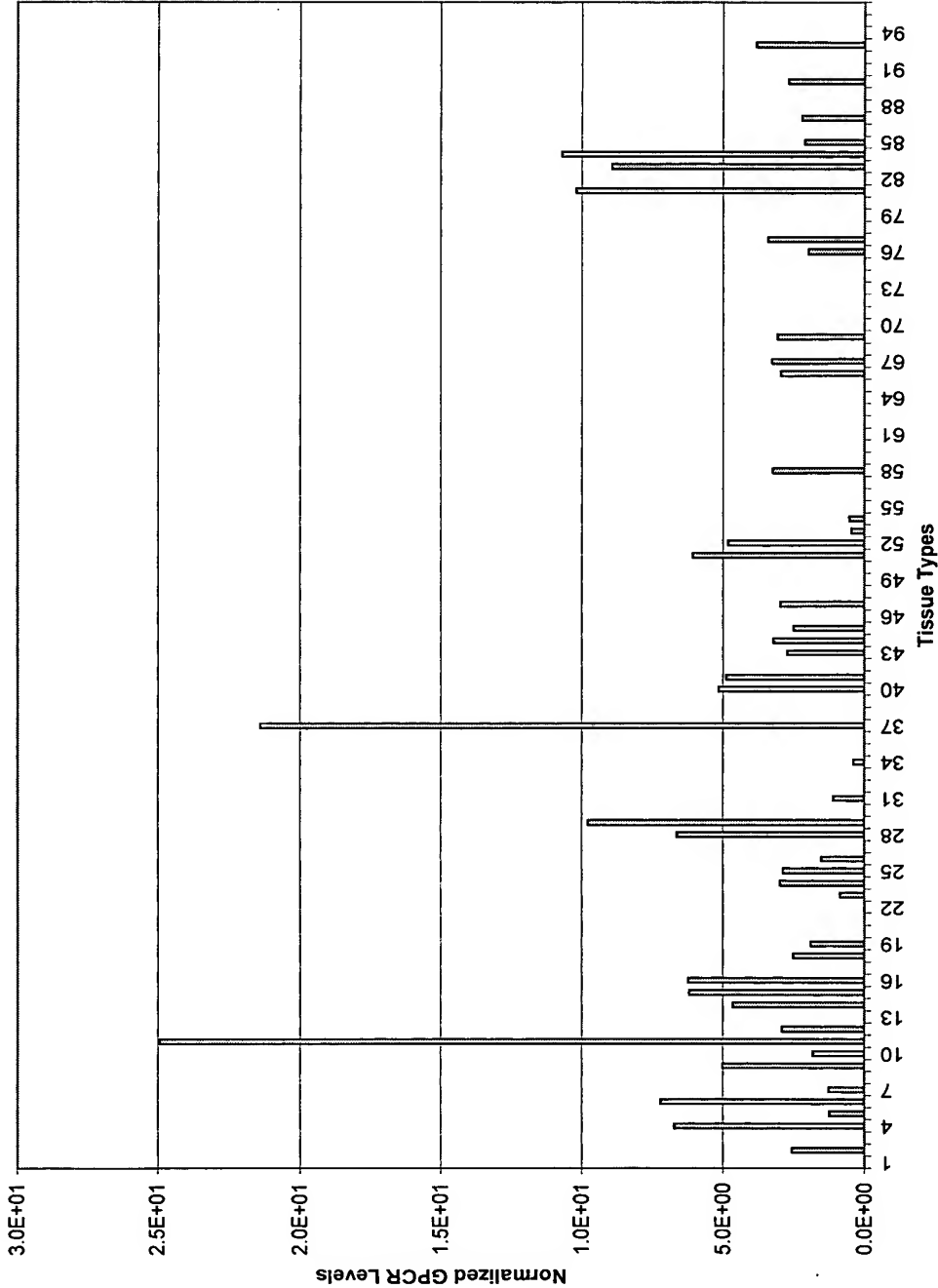


FIG. 17



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FIG. 18A

1	ATGACGTCCACCTGCACCAACAGCAGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC	60
1	M T S T C T N S T R E S N S S H T C M P	20
61	CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC	120
21	L S K M P I S L A H G I I R S T V L V I	40
121	TTCCTCGCCGCCTCTTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTTCAGCGCAAGCCG	180
41	F L A A S F V G N I V L A L V L Q R K P	60
181	CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG	240
61	Q L L Q V T N R F I F N L L V T D L L Q	80
241	ATTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCTCAAC	300
81	I S L V A P W V V A T S V P L F W P L N	100
301	AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTGCGCTTCGCCAGCGTCAAC	360
101	S H F C T A L V S L T H L F A F A S V N	120
361	ACCATTGTCNTGGTGTCACTGGATCGCTACTTGTCCATCATCCACCCTCTCTCTACCCG	420
121	T I V <u>X</u> V S V D R Y L S I I H P L S Y P	140
421	TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCTCTATGGCACCTGGATTGTGGCCATC	480
141	S K M T Q R R G Y L L L Y G T W I V A I	160
481	CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT	540
161	L Q S T P P L Y G W G Q A A F D E R N A	180
541	CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTTC	600
181	L C S M I W G A S P S Y T I L S V V S F	200
601	ATCGTCATTCCACTGATTGTTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCGG	660
201	I V I P L I V M I A C Y S V V F C A A R	220
661	AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC	720
221	R Q H A L L Y N V K R H S L E V R V K D	240
721	TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTCCAGGATGAGAGT	780
241	C V E N E D E E G A E K K E E F Q D E S	260
781	GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG	840
261	E F R R Q H E G E V K A K E G R M E A K	280
841	GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAAGTGAGAGTAGTGTAGAGGCC	900
281	D G S L K A K E G S T G T S E S S V E A	300

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FIG. 18B

901	AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT	960
301	R G S E E V R E S S T V A S D G S M E G	320
961	AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG	1020
321	K E G S T K V E E N S M K A D K G R T E	340
1021	GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC	1080
341	V N Q C S I D L G E D <u>X</u> M E F G E D D I	360
1081	AATTTCACTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCACCCAGTCGT	1140
361	N F S E D D V E A V N I P E S L P P S R	380
1141	CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTNNNAAGTG	1200
381	R N S N S N P P L P R C Y Q C K A <u>X</u> K V	400
1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTCAGCAGTC	1260
401	I F I I I F S Y V L S L G P Y C F L A V	420
1261	CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC	1320
421	L A V W V D V E T Q V P Q W V I T I I I	440
1321	TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC	1380
441	W L F F L Q C C I H P Y V Y G Y M H K T	460
1381	ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCGAAA	1440
461	I K K E I Q D M L K K F F C K E K P P K	480
1441	GAAGATAGCCACCCAGACCTGCCCCGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT	1500
481	E D S H P D L P G T E G G T E G K I V P	500
1501	TCCTACGATTCTGCTACTTTTCCTTGA	1527
501	S Y D S A T F P	508

FIG. 19

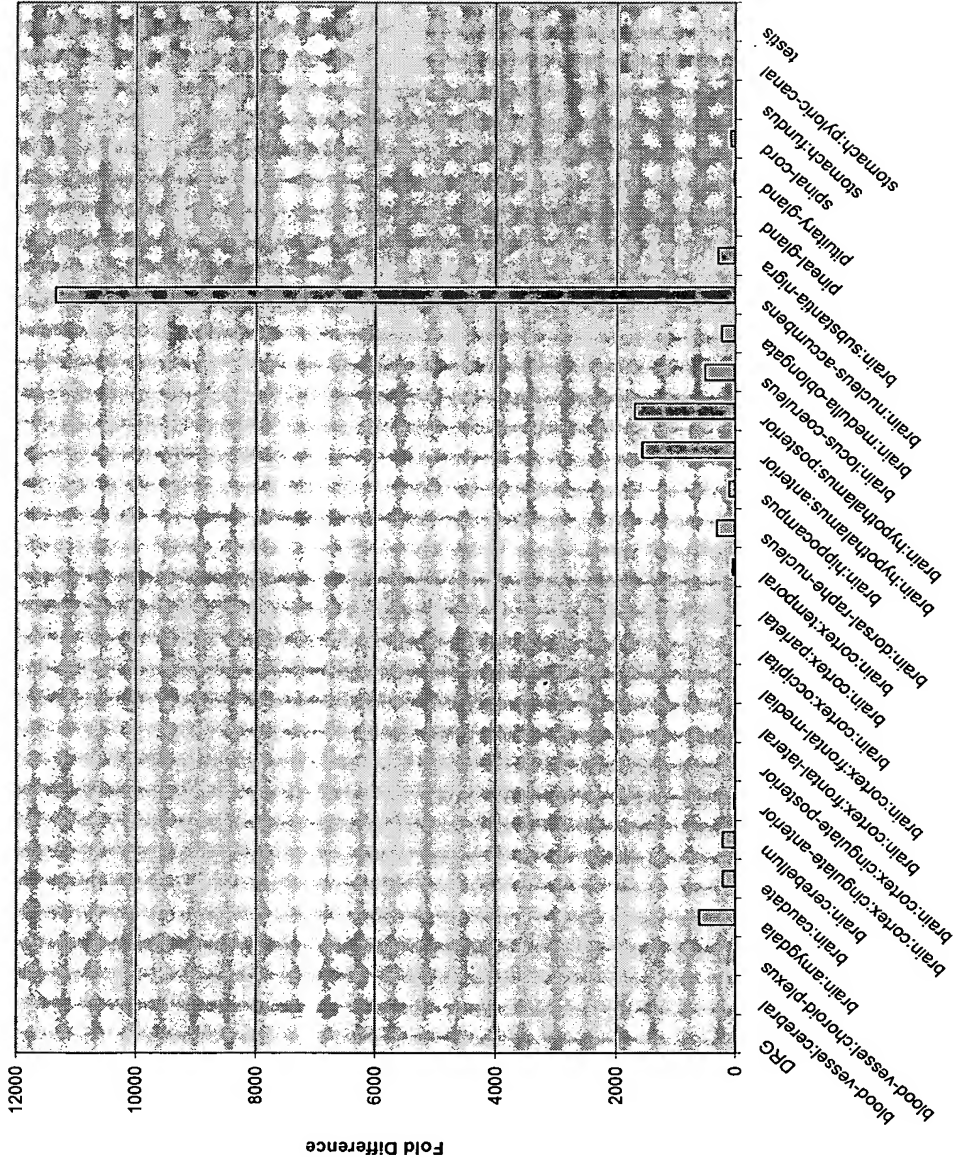
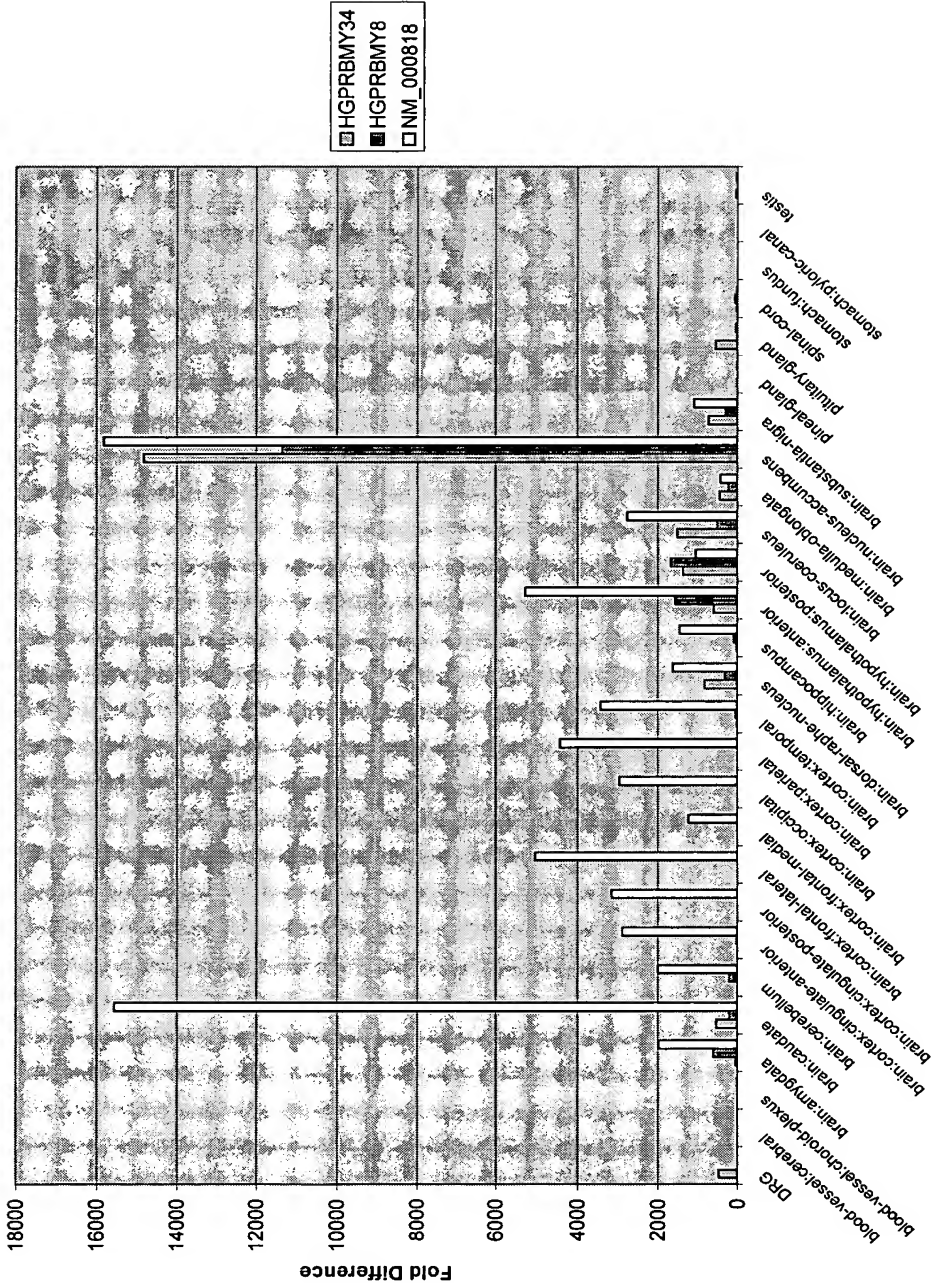


FIG. 20



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FIG. 21

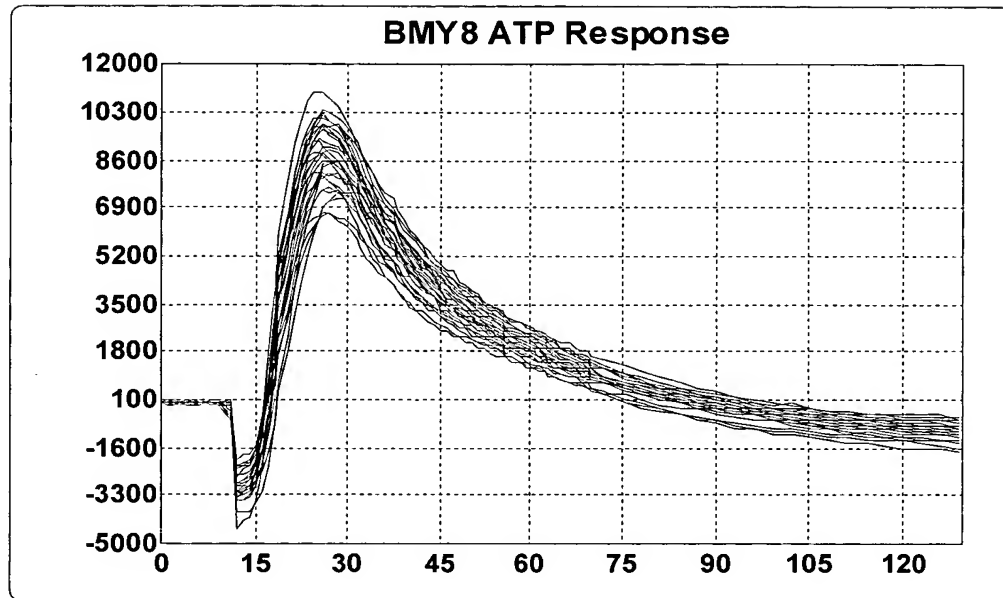


FIG. 22

